

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:17:40 ; Search time 71.77 Seconds
(without alignments)
27.514 Million cell updates/sec

Title: US-09-052-089a-5

Perfect score: 286
Sequence: 1 RALCTICSDPFDHSDVAA.....IOSFETAPSRICPCQRIQVG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	32.5	190	1 RNF4_HUMAN	P78317 homo sapien
2	93	32.5	194	1 RNF4_MOUSE	Q9QZS2 mus musculu
3	93	32.5	194	1 RNF4_RAT	O88846 rattus norv
4	92.5	32.3	624	1 A33_PLEVA	O02084 pleurodeles
5	88.5	30.9	411	1 RAPS_TORCA	P09108 torpedo cal
6	86	30.1	474	1 CBIC_HUMAN	O9ulv8 homo sapien
7	86	30.1	1238	1 YQO9_CAEEL	O09298 caenorhabdi
8	85.5	29.9	411	1 RAPS_CHICK	O42393 gallus gall
9	85.5	29.9	544	1 MKR3_MOUSE	O60764 mus musculu
10	84.5	29.5	411	1 RAPS_HUMAN	Q13702 homo sapien
11	84	29.4	513	1 REP_HUMAN	P14373 homo sapien
12	83.5	29.2	411	1 RAPS_MOUSE	P12672 mus musculu
13	83	29.0	235	1 YQ57_CAEEL	O09463 caenorhabdi
14	82	28.7	284	1 GOL1_DROME	O06003 drosophila
15	82	28.7	324	1 BM11_MOUSE	P25916 mus musculu
16	82	28.7	326	1 BM11_HUMAN	P35226 homo sapien
17	82	28.7	342	1 ME18_MOUSE	P33798 mus musculu
18	82	28.7	344	1 ME18_HUMAN	P35227 homo sapien
19	81.5	28.5	485	1 MKR4_HUMAN	Q13434 homo sapien
20	81	28.3	202	1 YP99_CAEEL	O09477 caenorhabdi
21	81	28.3	539	1 Z173_HUMAN	O12899 homo sapien
22	81	28.3	634	1 Z147_MOUSE	O61510 mus musculu
23	80	28.0	906	1 CBL_HUMAN	P32681 homo sapien
24	79.5	27.8	161	1 YQUD_CAEEL	P30631 caenorhabdi
25	79	27.6	632	1 Z179_HUMAN	Q9ulv5 homo sapien
26	78	27.3	1281	1 YLB5_CAEEL	P46560 caenorhabdi
27	77	26.9	522	1 REP_MOUSE	O62158 mus musculu
28	77	26.9	917	1 STE5_YEAST	P32917 saccharomyc
29	77	26.9	982	1 CBLB_HUMAN	O13191 homo sapien
30	76.5	26.9	416	1 MKR2_HUMAN	O9h000 homo sapien
31	76.5	26.7	416	1 MKR2_MOUSE	O9evr1 mus musculu
32	75.5	26.4	2025	1 TTC3_HUMAN	P33804 homo sapien
33	75	26.2	470	1 R052_MOUSE	O62191 mus musculu

34	75	26.2	631	1 Z179_RAT	O70418 rattus norv
35	73.5	25.7	409	1 YQ55_CAEEL	O09251 caenorhabdi
36	73.5	25.7	478	1 MKR1_MACEL	O9t191 macropus eu
37	73.5	25.7	481	1 MKR1_MOUSE	O9qxp6 mus musculu
38	73.5	25.7	482	1 MKR1_HUMAN	O9unc7 mus sapien
39	73.5	25.7	585	1 YHBO_YEAST	P38748 saccharomyc
40	73	25.5	600	1 RNL1_MOUSE	O9wlv7 mus musculu
41	73	25.5	1562	1 YM81_YEAST	O04781 saccharomyc
42	72	25.2	482	1 RNF9_HUMAN	O9udv6 homo sapien
43	72	25.2	489	1 RNF9_MOUSE	O9wv45 mus musculu
44	72	25.2	624	1 RNL2_HUMAN	O9wv42 homo sapien
45	72	25.2	1169	1 RAD5_YEAST	P32849 saccharomyc

ALIGNMENTS

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RESULT 1
ID      RNF4_HUMAN          STANDARD;          PRT;          190 AA.
AC      P78317;
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DE      RING finger protein 4.
GN      RNF4.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=98403881; PubMed=9734812;
RA      Hadano S., Ishida Y., Ikeda J.E.;
RT      "The primary structure and genomic organization of five novel
RT      transcripts located close to the Huntington's disease gene on human
RT      chromosome 4p16.3.";
RL      DNA Res. 5:177-186(1998).
RN      [2]
RP      SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RC      TISSUE=Brain;
RX      MEDLINE=98140125; PubMed=9479498;
RA      Chiarloti L., Benvenuto G., Fedele M., Santoro M., Simeone A.,
RT      Fusco A., Bruni C.B.;
RT      "Identification and characterization of a novel RING-finger gene
RT      (RNF4) mapping at 4p16.3.";
RL      Genomics 47:258-265(1998).
CC      -1- FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL
CC      ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION (BY
CC      SIMILARITY).
CC      -1- SUBUNIT: INTERACTS WITH GSK3, ANDROGEN RECEPTOR AND TBP (by
CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC      -1- TISSUE SPECIFICITY: WIDELY EXPRESSED AT LOW LEVELS IN MANY
CC      TISSUES; HIGHLY EXPRESSED IN TESTIS.
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      -----
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CC      -----
DR      EMBL; AB000468; BAA19122.1; -
DR      EMBL; U95140; AAC52022.1; -
DR      MIM; 602850; -
DR      InterPro: IPR001841; Znf_Ring.
DR      Pfam; PF00097; ZF-C3HC4; 1.
DR      SMART; SM00184; RING; 1.
DR      PROSITE; PS00518; ZF_RING_1; 1.

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DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Transcription regulation; Activator; Zinc-finger; Nuclear protein.
 FT ZN-FING 132 177 RING-TYPE.
 SO SEQUENCE 190 AA; 21319 MW; ESE3AE4A9B28CF9D CRC64;

Query Match 32.5%; Score 93; DB 1; Length 190;
 Best Local Similarity 37.3%; Pred. No. 7.4e-05;
 Matches 19; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

OY 4 CTC-----SDFPDHSDVAAMDCGHTFHLOCLIOSFETAPSPCTCQCRIOV 50
 DB 132 CPICMDGSEIVQNGRLIVSTECGHVFCSCQLRSLKNA--NTCPTCRKKI 180

RESULT 2
 ID RNF4_MOUSE STANDARD; PRT; 194 AA.
 AC 090252; 035941;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RING finger protein 4.
 GN RNF4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Embryo;
 RX MEDLINE=20284895; PubMed=10822263;
 RA Gallil N., Nayak S., Epstein J.A., Buck C.A.;
 RT "Rnf4, a RING protein expressed in the developing nervous and
 reproductive systems, interacts with Gsc1, a gene within the DGeorge
 critical region.";
 RT Dev. Dyn. 218:102-111(2000).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CS7BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Araiawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Steadli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 16-178 FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=98140125; PubMed=9479498;
 RA Chiarotti L., Benvenuto G., Fedele M., Santoro M., Simeone A.,
 RA Fusco A., Bruni C.B.;
 RT "Identification and characterization of a novel RING-finger gene
 (RNF4) mapping at 4p16.3.";

RL Genomics 47:258-265(1998).
 CC -1- ACTIVATION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL
 CC ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION (BY
 CC SIMILARITY)
 CC -1- SUBUNIT: INTERACTS WITH GSC1, ANDROGEN RECEPTOR AND TBP.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED PRIMARILY IN THE
 CC DEVELOPING NERVOUS SYSTEM WITH STRONG EXPRESSION IN THE DORSAL
 CC ROOT GANGLIA AND GONADS. UNBOUTHOUSLY EXPRESSED IN THE ADULT.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS DETECTED FROM EMBRYONIC DAY 7
 CC AND CONTINUES THROUGHOUT DEVELOPMENT AND INTO ADULTHOOD.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL; AF169330; AAF00620.1; -;
 DR EMBL; AK019171; BAB31585.1; -;
 DR EMBL; BC003282; AAH03282.1; -;
 DR EMBL; U95141; AAC53539.1; -;
 DR MGD; MGI:1201691; Rnf4.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam; PF00097; ZF-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Transcription regulation; Activator; Zinc-finger; Nuclear protein.
 FT ZN-FING 136 181 RING-TYPE.
 SO SEQUENCE 194 AA; 21910 MW; 9A0A4277725C62E5 CRC64;

Query Match 32.5%; Score 93; DB 1; Length 194;
 Best Local Similarity 37.3%; Pred. No. 7.6e-05;
 Matches 19; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

OY 4 CTC-----SDFPDHSDVAAMDCGHTFHLOCLIOSFETAPSPCTCQCRIOV 50
 DB 136 CPICMDGSEIVQNGRLIVSTECGHVFCSCQLRSLKNA--NTCPTCRKKI 184

RESULT 3
 ID RNF4_RAT STANDARD; PRT; 194 AA.
 AC 088846;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RING finger protein 4 (SNURF).
 GN RNF4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98378525; PubMed=9710597;
 RA Mollanen A.-M., Poukka H., Karvonen U., Hakli M., Janne O.A.,
 RA Palvimo J.U.;
 RT "Identification of a novel RING finger protein as a coregulator in
 RT steroid receptor-mediated gene transcription.";
 RT Mol. Cell. Biol. 18:5128-5139(1998).
 CC -1- FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL
 CC ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION.
 CC -1- SUBUNIT: INTERACTS WITH GSC1, ANDROGEN RECEPTOR AND TBP.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN
 CC TESTIS.

[illegible]

[illegible]

```

OX NCBI_TaxID=9606;
RN (1)
RN SEQUENCE FROM N.A. (LONG FORM).
RX MEDLINE=20035821; PubMed=10571044;
RA Kim M., Tezuka T., Suzuki Y., Sugano S., Hirai M., Yamamoto T.;
RT "Molecular cloning and characterization of a novel cbl-family gene,
RL cbl-C."
RL Gene 239:145-154(1999).
RN (12)
RN SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
RP TISSUE-Pancreatic adenocarcinoma;
RC MEDLINE=99289203; PubMed=10362357;
RA Keane M.M., Ettenberg S.A., Nau M.M., Banerjee P., Cuello M.,
RT Penninger J., Lipkowitz S.;
RL "cbl-3: a new mammalian cbl family protein."
CC Oncogene 18:3365-3375(1999).
CC -1- FUNCTION: REGULATOR OF EGFR MEDIATED SIGNAL TRANSDUCTION.
CC -1- SUBUNIT: INTERACTS WITH A RESTRICTED RANGE OF SH3 DOMAIN PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS (A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: BUBOUTOIDS.
CC -1- PTM: PHOSPHORYLATED ON TYROSINES BY EGFR.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: AB028645; BAA6298.1; -
DR EMBL: AF117646; AAD3434.1; -
DR EMBL: AF117647; AAD3434.2.1; -
DR HSSP: P22681; 1847.
DR InterPro: IPR003153; CBL_N.
DR InterPro: IPR000980; SH2.
DR Pfam: PF02262; CBL_N.1.
DR Pfam: PF02761; CBL_N2.1.
DR Pfam: PF02762; CBL_N3.1.
DR Pfam: PF00097; ZF-C3HC4.1.
DR SMART: SM00184; RING.1.
DR SMART: SM00252; SH2.1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS0089; ZF_RING_2; 1.
DR Nuclear protein; Zinc-finger; Phosphorylation; Alternative splicing.
KM DOMAIN 89 92
FT ZN_FING 351 390
FT VSPLIC 261 306
FT CONFLICT 234 234 MISSING (IN SHORT ISOFORM).
FT T -> N (IN REF. 2).
SQ SEQUENCE 474 AA; 52468 MW; 91013DDP12828242 CRC64;

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RA  Lloyd C.;
RL  Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
CC  -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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-----
CC  EMBL; 246787; CAAB6745.1; -
CC  Wormpep; C16C10.7; CE01498.
CC  InterPro; IPR000306; Znf_FYVE.
CC  InterPro; IPR001841; Znf_Ring.
CC  Pfam; PF000097; zf-C3HC4; 1.
CC  SMART; SM00064; FYVE; 1.
CC  SMART; SM00184; RING; 1.
CC  PROSITE; PS00518; ZF_RING_1; 1.
CC  PROSITE; PS50089; ZF_RING_2; 1.
CC  Hypothetical protein; Zinc-finger.
CC  ZN_FING 26 67 RING-TYPE.
CC  DOMAIN 121 124 POLY-GLY.
CC  FT 169 172
CC  SEQUENCE 235 AA; 24915 MW; 21A04AE951F6382A CRC64;

Query Match 29.08; Score 83; DB 1; Length 235;
Best Local Similarity 37.88; Pred. NO. 0.0017;
Matches 17; Conservative 6; Mismatches 18; Indels 4; Gaps 2;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLQCLIOSFETAP-SRTCPQCR 47
    ||| |::| ||| |::| ||| |::| ||| |::|
Db 26 CNIC---LDAAKDAVNSLCGHLFCMPCLSQMLDTRPNNOVCPCVK 67

RESULT 14
GOLI_DROME STANDARD; PRT; 284 AA.
ID G06003;
AC 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Goliah protein (G1 protein).
DE GOL OR G1 OR GL.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93216124; PubMed=8462875;
RA Boucharde M.L., Cote S.;
RT "The Drosophila melanogaster developmental gene g1 encodes a variant
RT zinc-finger-motif protein."
RL Gene 125:205-209(1993).
CC -1- FUNCTION: REGULATION OF GENE EXPRESSION DURING MESODERM FORMATION.
CC -1- PUTATIVE ROLE AS TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: VISCERAL MESODERM AND PRIMORDIA OF SOMATIC
CC MUSCULATURE.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC  EMBL; M97204; AAA28582.1; -
CC  PIR; JCI495; JCI495.
CC  FlyBase; FBgn0004919; gol.
CC  InterPro; IPR001841; Znf_Ring.
CC  Pfam; PF000097; zf-C3HC4; 1.
CC  SMART; SM00184; RING; 1.
CC  PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC  PROSITE; PS50089; ZF_RING_2; 1.
CC  Developmental protein; zinc-finger; transcription regulation;
CC  DNA-binding; Nuclear protein.
CC  ZN_FING 126 167 RING-TYPE.
CC  DOMAIN 208 259 GLN/PRO/SER-RICH.
CC  FT 284 AA; 31973 MW; ECCEZD5EEDBA1E2B CRC64;
CC  SEQUENCE 284 AA; 31973 MW; ECCEZD5EEDBA1E2B CRC64;

Query Match 28.78; Score 82; DB 1; Length 284;
Best Local Similarity 31.48; Pred. NO. 0.0027;
Matches 16; Conservative 8; Mismatches 17; Indels 10; Gaps 2;

OY 4 CTICSDFFDHSRDVAMDCGHTFHLQCLIOSFETAP-SRTCPQCR 50
    ||| |::| ||| |::| ||| |::| ||| |::|
Db 126 CALCIETAKPTDITRIILPCKEHFKNCIDPWLE-----HRTCPMKLDV 170

RESULT 15
BML_MOUSE STANDARD; PRT; 324 AA.
ID BML_MOUSE
AC P25916;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Polycarb complex protein BML-1.
DE BML OR BML-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91249382; PubMed=1904009;
RA Haupt Y., Alexander W.S., Barri G., Klinken S.P., Adams J.M.;
RT "Novel zinc finger gene implicated as myc collaborator by
RT retrovirally accelerated lymphomagenesis in E mu-myc transgenic
RT mice."
RL Cell 65:753-761(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91249381; PubMed=1904008;
RA van Lohuizen M., Verbeek S., Scheijen B., Mientjens E.,
RA Gulden H., Berns A.;
RT "Identification of cooperating oncogenes in E mu-myc transgenic mice
RT by provirus tagging."
RL Cell 65:737-752(1991).
CC -1- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
CC STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
CC IN ITS EXPRESSIBILITY.
CC -1- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
CC (PCG).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: DETECTED IN MOST ORGANS WITH HIGH EXPRESSION
CC LEVELS IN THYMUS, HEART, BRAIN AND TESTIS.
CC -1- DISEASE: COOPERATES WITH THE MYC ONCOGENE TO PRODUCE B LYMPHOMAS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-----
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DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 18.8 kDa protein ZK637.14 in chromosome III.
GN ZK637.14
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderridae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=92168156; PubMed=1536779;
RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
RA Halloran N., Green P., Thierry-Mieg J., Oiu L., Dear S., Coulson A.,
RA Craxton M., Dubin R.K., Berts M., Metzstein M., Hawkins T.,
RA Ainscough R., Waterston R.,
RT "The C. elegans genome sequencing project: a beginning.";
RL Nature 356:37-41(1992).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
CC EMBL: 211115; CAA77447.1; -.
CC PIR: S15788; S15788.
CC WormPep: ZK637.14; CE00432.
CC InterPro: IPR001841; Znf_fing.
CC Pfam: PF00097; zf-C3HC4; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC Hypothetical protein; zinc-finger.
CC ZN_FING 72 134 RING-TYPE.
CC SEQUENCE 161 AA; 18847 MW; F5EP9F3A83A9C027 CRC64;
SQ

Query Match 27.8%; Score 79.5; DB 1; Length 161;
Best Local Similarity 30.0%; Pred. No. 0.0032;
Matches 21; Conservative 4; Mismatches 22; Indels 23; Gaps 2;

QY 2 ALCTGSDPFDHSRD-----VAAMDCGTFHLQCLQSFEETAPS 40
DB 70 ATCAICIDNLDNNVDIEDHVKELKIDPTTGTCTVYVMPCKHRHFYCLTLWLEA--Q 127
OY 41 RTCPGCRIOV 50
DB 128 QTCTPTCKOKV 137

RESULT 25
ID 2179_HUMAN STANDARD; PRT; 632 AA.
AC Q9ULX5; O60633;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein 179 (Brain finger protein).
GN ZNF179 OR BFP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Seki N., Hattori A., Saito T.;
RT "Human BFP/ZNF179.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

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RN [2]
RP SEQUENCE OF 33-127 FROM N.A.
RX MEDLINE=96301415; PubMed=8660987;
RA Matsuda Y., Inoue S., Seki N., Hosoi T., Orimo A., Muramatsu M.,
RA Hori T.;
RT "Chromosome mapping of human (ZNF179), mouse, and rat genes for brain
RT finger protein (bfp), a member of the RING finger family.";
RL Genomics 33:325-327(1996).
CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AB026054; BAA84698.1; -.
CC DR EMBL: AF054587; AAC08584.1; -.
CC DR MIM: 601237; -.
CC DR InterPro: IPR001841; Znf_fing.
CC DR Pfam: PF00097; zf-C3HC4; 1.
CC DR SMART: SM00184; RING; 1.
CC DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC DR PROSITE: PS50089; ZF_RING_2; 1.
CC ZN_finger.
CC ZN_FING 57 98 RING-TYPE.
CC SEQUENCE 632 AA; 68354 MW; F8D294815E65ED02 CRC64;
SQ

Query Match 27.6%; Score 79; DB 1; Length 632;
Best Local Similarity 34.7%; Pred. No. 0.014;
Matches 17; Conservative 7; Mismatches 13; Indels 12; Gaps 3;

QY 4 CTTCSDPFDHSRDVAAMDCGTFHLQCLQSFEET-----APSRCPQCR 47
DB 57 CSIC---LERRDPISLDCGHDFCIRC-----FSHRRLPGCEPPCCPCR 98

RESULT 26
ID YLB5_CAEEL STANDARD; PRT; 1281 AA.
AC P46580;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 146.8 kDa protein C34E10.5 in chromosome III.
GN C34E10.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderridae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Kirsten J.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: TO S.POMBE SKB1 AND YEAST YBR133C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U10402; AAA19067.1; -.
CC DR WormPep: C34E10.5; CE01185.
CC DR InterPro: IPR001841; Znf_fing.

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DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein, Transmembrane; Zinc-finger.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 1165 1185 POTENTIAL.
FT ZN_FING 1222 1267 RING-TYPE.
SQ SEQUENCE 1281 AA; 146773 MW; 7027275AB8540D04 CRC64;

Query Match 27.3%; Score 78; DB 1; Length 1281;
Best Local Similarity 30.8%; Pred. No. 0.037;
Matches 16; Conservative 12; Mismatches 14; Indels 10; Gaps 2;

OY 4 CTICSDFFHSRDVYAMDCGTHFLQCLIQ-----SFETAPSRRCPCRCRQ 49
Db 1222 CSTCLE---NKNPSALFCGHLFCWTCIQEHAVATSSASTSSARCPQCRLE 1269

RESULT 27
REP_MOUSE STANDARD; PRT; 522 AA.
AC Q62158;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zinc-finger protein RFP (Ret finger protein).
GN RFP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=97176437; PubMed=9023983;
RA Cao T., Shannon M., Handel M.A., Etkin L.D.;
RT "Mouse ret finger protein (rfp) proto-oncogene is expressed at
RT specific stages of mouse spermatogenesis."
RL Dev. Genet. 19:309-320(1996).
CC -1- FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
-----
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FT ZN_FING 25 66 RING-TYPE.
FT ZN_FING 105 136 B BOX-TYPE.
FT DOMAIN 377 502 SPRY.
SQ SEQUENCE 522 AA; 59550 MW; BFD418DBA13340B7 CRC64;

Query Match 26.9%; Score 77; DB 1; Length 522;
Best Local Similarity 33.3%; Pred. No. 0.021;
Matches 15; Conservative 8; Mismatches 18; Indels 4; Gaps 2;

OY 4 CTICSDFFHSRDVYAMDCGTHFLQCLIQSEFAPSR-TCPCRCR 47
Db 25 CPVCLQYF---VEPMMLDCGNICACIARCGAETNVSCPCR 66

RESULT 28
STES_YEAST STANDARD; PRT; 917 AA.
AC P32917;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE STES protein.
GN STES OR NUL3 OR YDR103W OR YD8557.12.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93204951; PubMed=8455598;
RA Mukai Y., Harashima S., Oshima Y.;
RT "Function of the ste signal transduction pathway for mating
RT pheromones sustains MAT alpha 1 transcription in Saccharomyces
RT cerevisiae."
RL Mol. Cell. Biol. 13:2050-2060(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93296161; PubMed=8516289;
RA Perlman R., Yablonski D., Simchen G., Levitzki A.;
RT "Cloning of the STE5 gene of Saccharomyces cerevisiae as a suppressor
RT of the mating defect of cdc25 temperature-sensitive mutants."
RL Proc. Natl. Acad. Sci. U.S.A. 90:5474-5478(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Mckey V.L., Mathewes S., Bell L., O'Hara P.J.;
RL Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=DBG939;
RX MEDLINE=94067004; PubMed=8246877;
RA Lieberer E., Dignard D., Harscus D., Horgan L., Whiteway M.,
RA Thomas D.Y.;
RT "Cloning of Saccharomyces cerevisiae STE5 as a suppressor of a Ste20
RT protein kinase mutant: structural and functional similarity of Ste5
RT to Far1."
RL Mol. Gen. Genet. 241:241-254(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE PHEROMONE SIGNAL TRANSDUCTION PATHWAY.
CC IT MEDIATES PHEROMONE SIGNALS ACTING BETWEEN STE20 AND STE11.
CC IT IS ABSOLUTELY REQUIRED FOR PHEROMONE-INDUCED TRANSCRIPTION OF
CC FUS1. MAY PLAY A ROLE IN CELL-CYCLE ARREST IN RESPONSE TO
CC PHEROMONE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: MAY BE REGULATED AT THE PHOSPHORYLATION LEVEL, AND BY THE
CC MATING TYPE OF THE CELL AND DEPENDS ON AN INTACT PHEROMONE-
CC RESPONSE PATHWAY.
CC -1- SIMILARITY: TO YEAST FAR1.
-----
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RL Genome Res. 10:1546-1560(2000).
RN [3]
RP SEQUENCE OF 44-416 FROM N.A.
RC TISSUE-Eye;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC -----
DR EMBL: AF302084; AAC30426.1; -
DR EMBL: AF277170; AAC27595.1; -
DR EMBL: AF277164; AAC27595.1; JOINED.
DR EMBL: AF277165; AAC27595.1; JOINED.
DR EMBL: AF277166; AAC27595.1; JOINED.
DR EMBL: AF277167; AAC27595.1; JOINED.
DR EMBL: AF277168; AAC27595.1; JOINED.
DR EMBL: AF277169; AAC27595.1; JOINED.
DR EMBL: AF161555; AAC29042.2; -
DR EMBL: BC001799; AAH01799.1; -
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf-FING.
DR Pfam: PF00097; Zf-C3HC4; 4.
DR Pfam: PF00642; Zf-CCCH; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf-C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 8 C3H1-TYPE 1.
FT ZN_FING 37 C3H1-TYPE 2.
FT ZN_FING 171 C3H1-TYPE 3.
FT DOMAIN 193 222 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 238 292 RING-TYPE.
FT ZN_FING 327 347 C3H1-TYPE 4.
FT ZN_FING 327 347 F -> V (IN REF. 2 AND 3).
FT CONFLICT 186 186
FT CONFLICT 278 278 K -> E (IN REF. 2).
FT CONFLICT 278 278
SQ SEQUENCE 416 AA; 46988 MM; 02B6B7ABBD382DDC CRC64;

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Query Match 26.7%; Score 76.5; DB 1; Length 416;
Best Local Similarity 28.1%; Pred. No. 0.019;
Matches 16; Conservative 10; Mismatches 20; Indels 11; Gaps 2;
QY 3 LCTICSDFF-----DHSRDVAAMDCGTFHLOCLIO-----SETPASRTPCPCRI 48
Db 237 VCSICMEVILEKASASERRRFGILSNCHTYCLSCIRQWCAKQEPENFIKSPCCRV 293

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RESULT 31
MKR2_MOUSE STANDARD; PRT; 416 AA.
ID MKR2_MOUSE
AC Q9ERV1; Q9DOL9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 2.
GN MKR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21481893; PubMed=11597136;

```

```

RA Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.;
RT "Phylogenetic conservation of the makorin-2 gene, encoding a multiple
RT zinc-finger protein, antisense to the raf1 proto-oncogene.";
RL Genomics 77:119-126(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC -----
DR EMBL: AF277171; AAC27596.1; -
DR EMBL: AK011295; BAB27523.1; -
DR MGD: MGI:1914277; Mkrn2.
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf-FING.
DR Pfam: PF00097; Zf-C3HC4; 4.
DR Pfam: PF00642; Zf-CCCH; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf-C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 8 C3H1-TYPE 1.
FT ZN_FING 37 C3H1-TYPE 2.
FT ZN_FING 171 C3H1-TYPE 3.
FT DOMAIN 193 222 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 238 292 RING-TYPE.
FT ZN_FING 327 347 C3H1-TYPE 4.
FT ZN_FING 327 347 L -> F (IN REF. 2).
FT CONFLICT 181 181
FT CONFLICT 181 181
SQ SEQUENCE 416 AA; 46562 MM; 5F2686B9D9A6C9F CRC64;

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Query Match 26.7%; Score 76.5; DB 1; Length 416;
Best Local Similarity 28.1%; Pred. No. 0.019;
Matches 16; Conservative 10; Mismatches 20; Indels 11; Gaps 2;
QY 3 LCTICSDFF-----DHSRDVAAMDCGTFHLOCLIO-----SETPASRTPCPCRI 48
Db 237 VCSICMEVILEKASASERRRFGILSNCHTYCLSCIRQWCAKQEPENFIKSPCCRV 293

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RESULT 32
TTTC3_HUMAN STANDARD; PRT; 2025 AA.
ID TTTC3_HUMAN

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DR EMBL: AF192793; AAF18979.1; -.
DR EMBL: AF192789; AAF18979.1; JOINED.
DR EMBL: AF192790; AAF18979.1; JOINED.
DR EMBL: AF192791; AAF18979.1; JOINED.
DR EMBL: AF192792; AAF18979.1; JOINED.
DR EMBL: AL136812; CAB66746.1; -.
DR InterPro: IPR000571; Znf-CCCH.
DR InterPro: IPR001841; Znf-CCCH.
DR Pfam: PF00097; Zf-CCCH; 1.
DR Pfam: PF00642; Zf-CCCH; 4.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger Repeat; Polymorphism.
KW ZN_FING 61 79 C3H1-TYPE 1.
FT ZN_FING 90 108 C3H1-TYPE 2.
FT ZN_FING 214 232 C3H1-TYPE 3.
FT DOMAIN 236 263 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 281 335 RING-TYPE.
FT ZN_FING 370 390 C3H1-TYPE 4.
FT VARIANT 243 243 L->V.
FT CONFLICT 395 396 /FTID-VAR_012161.
FT SEQUENCE 482 AA; 53363 MW; C993DECDD131691C CRC64;

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Query Match 25.7%; Score 73.5; DB 1; Length 482;
Best Local Similarity 28.1%; Pred. No. 0.052;
Matches 16; Conservative 11; Mismatches 19; Indels 11; Gaps 2;

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QY 3 LCTICSDFF-----DHSRDVAAMDCHTFLDCL-----IQSEPTASRTCPQCR 48
Db 280 VCGICMEVVEKANKNSERRRPFILSCNHTYCLCKIRKRSKQKPFESKIKSCPECR 336

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RESULT 39
YHBO_YEAST STANDARD; PRT: 585 AA.
AC P38748;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 67.5 kDa protein in PRPS4-STE20 intergenic region.
GN YH1010C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Galtun S., Gelsel C., Kirsten J.,
RA Kicaba T., Hillier L., Jiler M., Johnston L., Langston Y.,
RA Lettrelle P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Travaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -1- SIMILARITY: TO C.ELEGANS EED8.9 AND S.POMBE SPAC1658.13.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC EMBL: U11582; CAB34905.1; -.
DR PIR: S46825; S46825.
DR SGD: S0001002; YH1010C.
DR InterPro: IPR001841; Znf_fing.
DR InterPro: IPR001607; Zf-UBP.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR Pfam: PF02148; Zf-UBP; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00280; Znf-UBP; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE-NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Zinc-finger.
FT ZN_FING 240 280 RING-TYPE.
FT SEQUENCE 585 AA; 67503 MW; 88F670CC73A1263 CRC64;

```

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Query Match 25.7%; Score 73.5; DB 1; Length 585;
Best Local Similarity 33.3%; Pred. No. 0.063;
Matches 15; Conservative 6; Mismatches 19; Indels 5; Gaps 2;

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QY 4 CTICSDFFD-HSRDVAAMDCHTFLDCLIOSFETASRTCPQCR 47
Db 240 CPVCLERMDSFTGLVTPCQHTFHCOCL---NKKMSRCPVCR 280

```

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RESULT 40
RN12_MOUSE STANDARD; PRT: 600 AA.
AC Q9WTV7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RING finger protein 12 (LIM domain interacting RING finger protein)
DE (RING finger LIM domain-binding protein) (R-LIM).
GN RNF12 OR LIM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bach I.;
RT "Opposing developmental functions of positive and negative
RT coregulators of LIM homeodomain factors."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP FUNCTION.
RX MEDLINE=9364422; PubMed=10431247;
RA Bach I., Rodriguez-Esteban C., Carriere C., Bhushan A., Krones A.,
RA Rose D.W., Glass C.K., Andersen B., Izpisua Belmonte J.C.,
RA Rosenfeld M.G.;
RT "RIM inhibits functional activity of LIM homeodomain transcription
RT factors via recruitment of the histone deacetylase complex."
RL Nat. Genet. 22:394-399(1999).
CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN
CC TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE
CC DEACETYLASE COREPRESSOR COMPLEX.
CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch.)
CC -----
CC EMBL: AF069992; MAD34209.1; -.
DR MGD: MG1:1342291; Rnf12.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; Zf-C3HC4; 1.

```

DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Transcription regulation; zinc-finger.
 FT DOMAIN 415 484 SER-RICH.
 FT ZN_FING 546 587 RING-TYPE.
 FT DOMAIN 447 461 POLY-SER.
 SQ SEQUENCE 600 AA; 66470 MW; E68299530126E41D CRC64;

Query Match 25.5%; Score 73; DB 1; Length 600;
 Best Local Similarity 27.3%; Pred. No. 0.075;
 Matches 12; Conservative 10; Mismatches 20; Indels 2; Gaps 1;

Oy 4 CTICSDFFDHSRDVAMDCGHTFHQCLIQSFETAPSRTPQCR 47
 |::| : : | | | : | : | | | |
 Db 546 CSVCTEYEGDKLRKLPCHSHFVHCIDRWL--SENSTCPICR 587

Search completed: September 4, 2002, 16:17:41
 Job time: 500 sec

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